

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ANDERTON, STEPHEN MARK
VAN DER ZEE, RUURD
VAN EDEN, WILLEM

(ii) TITLE OF INVENTION: PEPTIDE FRAGMENTS OF MICROBIAL STRESS
PROTEINS AND PHARMACEUTICAL COMPOSITION MADE THEREOF FOR THE
TREATMENT AND PREVENTION OF INFLAMMATORY DISEASES

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: THE WEBB LAW FIRM

(B) STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE

(C) CITY: PITTSBURGH

(D) STATE: PENNSYLVANIA

(E) COUNTRY: UNITED STATES OF AMERICA

(F) ZIP: 15219-1818

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" FLOPPY DISK

(B) COMPUTER: DIGITAL VENTURIS GL 6200

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: MICROSOFT WORD 2.0c

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/716,169

(B) FILING DATE: 18-SEP-1996

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/NL95/00108

(B) FILING DATE: 21-MAR-1995

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu
1 5 10 15

Glu Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu
20 25 30

Gly Pro Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala
35 40 45

Pro Thr Ile Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu
50 55 60

Leu Glu Asp Pro Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu
65 70 75

Val Ala Lys Lys Thr Asp Asp Val Ala Gly Asp Gly Thr Thr Thr
80 85 90

Ala Thr Val Leu	Ala Gln Ala Leu Val	Arg Glu Gly Leu Arg Asn	95	100	105
Val Ala Ala Gly	Ala Asn Pro Leu Gly	Val Lys Arg Gly Ile Glu	110	115	120
Lys Ala Val Glu	Lys Val Thr Glu Thr	Leu Leu Lys Gly Ala Lys	125	130	135
Glu Val Glu Thr	Lys Glu Gln Ile Ala	Ala Thr Ala Ala Ile Ser	140	145	150
Ala Gly Asp Gln	Ser Ile Gly Asp Leu	Ile Ala Glu Ala Met Asp	155	160	165
Lys Val Gly Asn	Glu Gly Val Ile Thr	Val Glu Glu Ser Asn Thr	170	175	180
Phe Gly Leu Gln	Leu Glu Leu Thr Glu	Gly Met Arg Phe Asp Lys	185	190	195
Gly Tyr Ile Ser	Gly Tyr Phe Val Thr	Asp Pro Glu Arg Gln Glu	200	205	210
Ala Val Leu Glu	Asp Pro Tyr Ile Leu	Leu Val Ser Ser Lys Val	215	220	225
Ser Thr Val Lys	Asp Leu Leu Pro Leu	Leu Glu Lys Val Ile Gly	230	235	240
Ala Gly Lys Pro	Leu Leu Ile Ile Ala	Glu Asp Val Glu Gly Glu	245	250	255
Ala Leu Ser Thr	Leu Val Val Asn Lys	Ile Arg Gly Thr Phe Lys	260	265	270
Ser Val Ala Val	Lys Ala Pro Gly Phe	Gly Asp Arg Arg Lys Ala	275	280	285
Met Leu Gln Asp	Met Ala Ile Leu Thr	Gly Gly Gln Val Ile Ser	290	295	300
Glu Glu Val Gly	Leu Thr Leu Glu Asn	Ala Asp Leu Ser Leu Leu	305	310	315
Gly Lys Ala Arg	Lys Val Val Val Thr	Lys Asp Glu Thr Thr Ile	320	325	330
Val Glu Gly Ala	Gly Asp Thr Asp Ala	Ile Ala Gly Arg Val Ala	335	340	345

Gln	Ile	Arg	Gln	Glu	Ile	Glu	Asn	Ser	Asp	Ser	Asp	Tyr	Asp	Arg	350	355	360
Glu	Lys	Leu	Gln	Glu	Arg	Leu	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	365	370	375
Val	Ile	Lys	Ala	Gly	Ala	Ala	Thr	Glu	Val	Glu	Leu	Lys	Glu	Arg	380	385	390
Lys	His	Arg	Ile	Glu	Asp	Ala	Val	Arg	Asn	Ala	Lys	Ala	Ala	Val	395	400	405
Glu	Glu	Gly	Ile	Val	Ala	Gly	Gly	Gly	Val	Thr	Leu	Leu	Gln	Ala	410	415	420
Ala	Pro	Thr	Leu	Asp	Glu	Leu	Lys	Leu	Glu	Gly	Asp	Glu	Ala	Thr	425	430	435
Gly	Ala	Asn	Ile	Val	Lys	Val	Ala	Leu	Glu	Ala	Pro	Leu	Lys	Gln	440	445	450
Ile	Ala	Phe	Asn	Ser	Gly	Leu	Glu	Pro	Gly	Val	Val	Ala	Glu	Lys	455	460	465
Val	Arg	Asn	Leu	Pro	Ala	Gly	His	Gly	Leu	Asn	Ala	Gln	Thr	Gly	470	475	480
Val	Lys	Glu	Asp	Leu	Leu	Ala	Ala	Gly	Val	Ala	Asp	Pro	Val	Lys	485	490	495
Val	Thr	Arg	Ser	Ala	Leu	Gln	Asn	Ala	Ala	Ser	Ile	Ala	Gly	Leu	500	505	510
Phe	Leu	Thr	Thr	Glu	Ala	Val	Val	Ala	Asp	Lys	Pro	Glu	Lys	Glu	515	520	525
Lys	Ala	Ser	Val	Pro	Gly	Gly	Gly	Asp	Met	Gly	Gly	Met	Asp	Phe	530	535	540

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala	Val	Lys	Val	Gly	Ile	Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Asn	1	5	10	15
Val	Phe	Arg	Ala	Ala	Leu	Lys	Asn	Pro	Asp	Ile	Glu	Val	Val	Ala	20	25	30	

Val	Asn	Asp	Leu	Thr	Asp	Ala	Asn	Thr	Leu	Ala	His	Leu	Leu	Lys	35	40	45
Tyr	Asp	Ser	Val	His	Gly	Arg	Leu	Asp	Ala	Glu	Val	Ser	Val	Asn	50	55	60
Gly	Asn	Asn	Leu	Val	Val	Asn	Gly	Lys	Glu	Ile	Ile	Val	Lys	Ala	65	70	75
Glu	Arg	Asp	Pro	Glu	Asn	Leu	Ala	Trp	Gly	Glu	Ile	Gly	Val	Asp	80	85	90
Ile	Val	Val	Glu	Ser	Thr	Gly	Arg	Phe	Thr	Lys	Arg	Glu	Asp	Ala	95	100	105
Ala	Lys	His	Leu	Glu	Ala	Gly	Ala	Lys	Lys	Val	Ile	Ile	Ser	Ala	110	115	120
Pro	Ala	Lys	Asn	Glu	Asp	Ile	Thr	Ile	Val	Met	Gly	Val	Asn	Gln	125	130	135
Asp	Lys	Tyr	Asp	Pro	Lys	Ala	His	His	Val	Ile	Ser	Asn	Ala	Ser	140	145	150
Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	Phe	Ala	Lys	Val	Leu	His	Glu	155	160	165
Gln	Phe	Gly	Ile	Val	Arg	Gly	Met	Met	Thr	Thr	Val	His	Ser	Tyr	170	175	180
Thr	Asn	Asp	Gln	Arg	Ile	Leu	Asp	Leu	Pro	His	Lys	Asp	Leu	Arg	185	190	195
Arg	Ala	Arg	Ala	Ala	Ala	Glu	Ser	Ile	Ile	Pro	Thr	Thr	Thr	Gly	200	205	210
Ala	Ala	Lys	Ala	Val	Ala	Leu	Val	Leu	Pro	Glu	Leu	Lys	Gly	Lys	215	220	225
Leu	Asn	Gly	Met	Ala	Met	Arg	Val	Pro	Thr	Pro	Asn	Val	Ser	Val	230	235	240
Val	Asp	Leu	Val	Ala	Glu	Leu	Glu	Lys	Glu	Val	Thr	Val	Glu	Glu	245	250	255
Val	Asn	Ala	Ala	Leu	Lys	Ala	Ala	Ala	Glu	Gly	Glu	Leu	Lys	Gly	260	265	270
Ile	Leu	Ala	Tyr	Ser	Glu	Glu	Pro	Leu	Val	Ser	Arg	Asp	Tyr	Asn	275	280	285

Gly	Ser	Thr	Val	Ser	Ser	Thr	Ile	Asp	Ala	Leu	Ser	Thr	Met	Val
				290					295					300

Ile	Asp	Gly	Lys	Met	Val	Lys	Val	Val	Ser	Trp	Tyr	Asp	Asn	Glu
				305					310					315

Thr	Gly	Tyr	Ser	His	Arg	Val	Val	Asp	Leu	Ala	Ala	Tyr	Ile	Ala
				320					325					330

Ser Lys Gly

(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Val	Lys	Val	Gly	Val	Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Leu	Val
1				5					10					15

Thr	Arg	Ala	Ala	Phe	Ser	Cys	Asp	Lys	Val	Asp	Ile	Val	Ala	Ile
				20					25					30

Asn	Asp	Pro	Phe	Ile	Asp	Leu	Asn	Tyr	Met	Val	Tyr	Met	Phe	Gln
				35					40					45

Tyr	Asp	Ser	Thr	His	Gly	Lys	Phe	Asn	Gly	Thr	Val	Lys	Ala	Glu
				50					55					60

Asn	Gly	Lys	Leu	Val	Ile	Asn	Gly	Lys	Pro	Ile	Thr	Ile	Phe	Gln
				65					70					75

Glu	Arg	Asp	Pro	Val	Lys	Ile	Lys	Trp	Gly	Asp	Ala	Gly	Ala	Glu
				80					85					90

Tyr	Val	Val	Glu	Ser	Thr	Gly	Val	Phe	Thr	Thr	Met	Glu	Lys	Ala
				95					100					105

Gly	Ala	His	Leu	Lys	Gly	Gly	Ala	Lys	Arg	Val	Ile	Ile	Ser	Ala
				110					115					120

Pro	Ser	Ala	Asp	Ala	Pro	Met	Phe	Val	Met	Gly	Val	Asn	His	Glu
				125					130					135

Lys	Tyr	Asp	Asn	Ser	Leu	Lys	Ile	Val	Ser	Asn	Ala	Ser	Cys	Thr
				140					145					150

Thr	Asn	Cys	Leu	Ala	Pro	Leu	Ala	Lys	Val	Ile	His	Asp	Asn	Phe
				155					160					165

Gly Ile Val Glu	Gly Leu Met Thr Thr	Val His Ala Ile Thr	Ala
170		175	180
Thr Gln Lys Thr	Val Asp Gly Pro Ser	Gly Lys Leu Trp Arg	Asp
185		190	195
Gly Arg Gly Ala	Ala Gln Asn Ile Ile	Pro Ala Ser Thr Gly	Ala
200		205	210
Ala Lys Ala Val	Gly Lys Val Ile Pro	Glu Leu Asn Gly Lys	Leu
215		220	225
Thr Gly Met Ala	Phe Arg Val Pro Thr	Pro Asn Val Ser Val	Val
230		235	240
Asp Leu Thr Cys	Arg Leu Glu Lys Pro	Ala Lys Tyr Asp Asp	Ile
245		250	255
Lys Lys Val Val	Lys Gln Ala Ala Glu	Gly Pro Leu Lys Gly	Ile
260		265	270
Leu Gly Tyr Thr	Glu Asp Gln Val Val	Ser Cys Asp Phe Asn	Ser
275		280	285
Asn Ser His Ser	Ser Thr Phe Asp Ala	Gly Ala Gly Ile Ala	Leu
290		295	300
Asn Asp Asn Ile	Val Lys Leu Ile Ser	Trp Tyr Asp Asn Glu	Tyr
305		310	315
Gly Tyr Ser Asn	Arg Val Val Asp Leu	Met Ala Tyr Met Ala	Ser
320		325	330

Lys Glu

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Leu Arg Leu Pro Thr Val Phe Arg	Gln Met Arg Pro Val Ser
1	5 10 15
Arg Val Leu Ala Pro His Leu Thr Arg	Ala Tyr Ala Lys Asp Val
20	25 30
Lys Phe Gly Ala Asp Ala Arg Ala Leu	Met Leu Gln Gly Val Asp
35	40 45

Leu	Leu	Ala	Asp	Ala	Val	Ala	Val	Thr	Met	Gly	Pro	Lys	Gly	Arg	50	55	60
Thr	Val	Ile	Ile	Glu	Gln	Ser	Trp	Gly	Ser	Pro	Lys	Val	Thr	Lys	65	70	75
Asp	Gly	Val	Thr	Val	Ala	Lys	Ser	Ile	Asp	Leu	Lys	Asp	Lys	Tyr	80	85	90
Lys	Asn	Ile	Gly	Ala	Lys	Leu	Val	Gln	Asp	Val	Ala	Asn	Asn	Thr	95	100	105
Asn	Glu	Glu	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	110	115	120
Arg	Ser	Ile	Ala	Lys	Glu	Gly	Phe	Glu	Lys	Ile	Ser	Lys	Gly	Ala	125	130	135
Asn	Pro	Val	Glu	Ile	Arg	Arg	Gly	Val	Met	Leu	Ala	Val	Asp	Ala	140	145	150
Val	Ile	Ala	Glu	Leu	Lys	Lys	Gln	Ser	Lys	Pro	Val	Thr	Thr	Pro	155	160	165
Glu	Glu	Ile	Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Gly	Asp	Lys	170	175	180
Glu	Ile	Gly	Asn	Ile	Ile	Ser	Asp	Ala	Met	Lys	Lys	Val	Gly	Arg	185	190	195
Lys	Gly	Val	Ile	Thr	Val	Lys	Asp	Gly	Lys	Thr	Leu	Asn	Asp	Glu	200	205	210
Leu	Glu	Ile	Ile	Glu	Gly	Met	Lys	Phe	Asp	Arg	Gly	Tyr	Ile	Ser	215	220	225
Pro	Tyr	Phe	Ile	Asn	Thr	Ser	Lys	Gly	Gln	Lys	Cys	Glu	Phe	Gln	230	235	240
Asp	Ala	Tyr	Val	Leu	Leu	Ser	Glu	Lys	Lys	Ile	Ser	Ser	Ile	Gln	245	250	255
Ser	Ile	Val	Pro	Ala	Leu	Glu	Ile	Ala	Asn	Ala	His	Arg	Lys	Pro	260	265	270
Leu	Val	Ile	Ile	Ala	Glu	Asp	Val	Asp	Gly	Glu	Ala	Leu	Ser	Thr	275	280	285
Leu	Val	Leu	Asn	Arg	Leu	Lys	Val	Gly	Leu	Gln	Val	Val	Ala	Val	290	295	300

Lys	Ala	Pro	Gly	Phe	Gly	Asp	Asn	Arg	Lys	Asn	Gln	Leu	Lys	Asp	305	310	315
Met	Ala	Ile	Ala	Thr	Gly	Gly	Ala	Val	Phe	Gly	Glu	Glu	Gly	Leu	320	325	330
Thr	Leu	Asn	Leu	Glu	Asp	Val	Gln	Pro	His	Asp	Leu	Gly	Lys	Val	335	340	345
Gly	Glu	Val	Ile	Val	Thr	Lys	Asp	Asp	Ala	Met	Leu	Leu	Lys	Gly	350	355	360
Lys	Gly	Asp	Lys	Ala	Gln	Ile	Glu	Lys	Arg	Ile	Gln	Glu	Ile	Ile	365	370	375
Glu	Gln	Leu	Asp	Val	Thr	Thr	Ser	Glu	Tyr	Glu	Lys	Glu	Lys	Leu	380	385	390
Asn	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Asp	Gly	Val	Ala	Val	Leu	Lys	395	400	405
Val	Gly	Gly	Thr	Ser	Asp	Val	Glu	Val	Asn	Glu	Lys	Lys	Asp	Arg	410	415	420
Val	Thr	Asp	Ala	Leu	Asn	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	425	430	435
Ile	Val	Leu	Gly	Gly	Gly	Cys	Ala	Leu	Leu	Arg	Cys	Ile	Pro	Ala	440	445	450
Leu	Asp	Ser	Leu	Thr	Pro	Ala	Asn	Glu	Asp	Gln	Lys	Ile	Gly	Ile	455	460	465
Glu	Ile	Ile	Lys	Arg	Thr	Leu	Lys	Ile	Pro	Ala	Met	Thr	Ile	Ala	470	475	480
Lys	Asn	Ala	Gly	Val	Glu	Gly	Ser	Leu	Ile	Val	Glu	Lys	Ile	Met	485	490	495
Gln	Ser	Ser	Ser	Glu	Val	Gly	Tyr	Asp	Ala	Met	Ala	Gly	Asp	Phe	500	505	510
Val	Asn	Met	Val	Glu	Lys	Gly	Ile	Ile	Asp	Pro	Thr	Lys	Val	Val	515	520	525
Arg	Thr	Ala	Leu	Leu	Asp	Ala	Ala	Gly	Val	Ala	Ser	Leu	Leu	Thr	530	535	540
Thr	Ala	Glu	Val	Val	Val	Thr	Glu	Ile	Pro	Lys	Glu	Glu	Lys	Asp	545	550	555

Pro Gly Met Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly
560 565 570

Gly Met Phe

- (6) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 547
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: UNKNOWN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Ala	Lys	Asp	Val	Lys	Phe	Gly	Ala	Asp	Ala	Arg	Ala	Leu	Met	Leu	1	5	10	15
Gln	Gly	Val	Asp	Leu	Leu	Ala	Asp	Ala	Val	Ala	Val	Thr	Met	Gly	20	25	30	
Pro	Lys	Gly	Arg	Thr	Val	Ile	Ile	Glu	Gln	Ser	Trp	Gly	Ser	Pro	35	40	45	
Lys	Val	Thr	Lys	Asp	Gly	Val	Thr	Val	Ala	Lys	Ser	Ile	Asp	Leu	50	55	60	
Lys	Asp	Lys	Tyr	Lys	Asn	Ile	Gly	Ala	Lys	Leu	Val	Gln	Asp	Val	65	70	75	
Ala	Asn	Asn	Thr	Asn	Glu	Glu	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	80	85	90	
Thr	Val	Leu	Ala	Arg	Ser	Ile	Ala	Lys	Glu	Gly	Phe	Glu	Lys	Ile	95	100	105	
Ser	Lys	Gly	Ala	Asn	Pro	Val	Glu	Ile	Arg	Arg	Gly	Val	Met	Leu	110	115	120	
Ala	Val	Asp	Ala	Val	Ile	Ala	Glu	Leu	Lys	Lys	Gln	Ser	Lys	Pro	125	130	135	
Val	Thr	Thr	Pro	Glu	Glu	Ile	Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala	140	145	150	
Asn	Gly	Asp	Lys	Asp	Ile	Gly	Asn	Ile	Ile	Ser	Asp	Ala	Met	Lys	155	160	165	
Lys	Val	Gly	Arg	Lys	Gly	Val	Ile	Thr	Val	Lys	Asp	Gly	Lys	Thr	170	175	180	
Leu	Asn	Asp	Glu	Leu	Glu	Ile	Ile	Glu	Gly	Met	Lys	Phe	Asp	Arg	185	190	195	

Gly	Tyr	Ile	Ser	Pro	Tyr	Phe	Ile	Asn	Thr	Ser	Lys	Gly	Gln	Lys	200	205	210
Cys	Glu	Phe	Gln	Asp	Ala	Tyr	Val	Leu	Leu	Ser	Glu	Lys	Lys	Ile	215	220	225
Ser	Ser	Val	Gln	Ser	Ile	Val	Pro	Ala	Leu	Glu	Ile	Ala	Asn	Ala	230	235	240
His	Arg	Lys	Pro	Leu	Val	Ile	Ile	Ala	Glu	Asp	Val	Asp	Gly	Glu	245	250	255
Ala	Leu	Ser	Thr	Leu	Val	Leu	Asn	Arg	Leu	Lys	Val	Gly	Leu	Gln	260	265	270
Val	Val	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Asn	Arg	Lys	Asn	275	280	285
Gln	Leu	Lys	Asp	Met	Ala	Ile	Ala	Thr	Gly	Gly	Ala	Val	Phe	Gly	290	295	300
Glu	Glu	Gly	Leu	Asn	Leu	Asn	Leu	Glu	Asp	Val	Gln	Ala	His	Asp	305	310	315
Leu	Gly	Lys	Val	Gly	Glu	Val	Ile	Val	Thr	Lys	Asp	Asp	Ala	Met	320	325	330
Leu	Leu	Lys	Gly	Lys	Gly	Asp	Lys	Ala	His	Ile	Glu	Lys	Arg	Ile	335	340	345
Gln	Glu	Ile	Thr	Glu	Gln	Leu	Asp	Ile	Thr	Thr	Ser	Glu	Tyr	Glu	350	355	360
Lys	Glu	Lys	Leu	Asn	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Asp	Gly	Val	365	370	375
Ala	Val	Leu	Lys	Val	Gly	Gly	Thr	Ser	Asp	Val	Glu	Val	Asn	Glu	380	385	390
Lys	Lys	Asp	Arg	Val	Thr	Asp	Ala	Leu	Asn	Ala	Thr	Arg	Ala	Ala	395	400	405
Val	Glu	Glu	Gly	Ile	Val	Leu	Gly	Gly	Gly	Cys	Ala	Leu	Leu	Arg	410	415	420
Cys	Ile	Pro	Ala	Leu	Asp	Ser	Leu	Lys	Pro	Ala	Asn	Glu	Asp	Gln	425	430	435
Lys	Ile	Gly	Ile	Glu	Ile	Ile	Lys	Arg	Ala	Leu	Lys	Ile	Pro	Ala	440	445	450

Met	Thr	Ile	Ala	Lys	Asn	Ala	Gly	Val	Glu	Gly	Ser	Leu	Ile	Val
				455					460					465
Glu	Lys	Ile	Leu	Gln	Ser	Ser	Ser	Glu	Val	Gly	Tyr	Asp	Ala	Met
				470					475					480
Leu	Gly	Asp	Phe	Val	Asn	Met	Val	Glu	Lys	Gly	Ile	Ile	Asp	Pro
				485					490					495
Thr	Lys	Val	Val	Arg	Thr	Ala	Leu	Leu	Asp	Ala	Ala	Gly	Val	Ala
				500					505					510
Ser	Leu	Leu	Thr	Thr	Ala	Glu	Ala	Val	Val	Thr	Glu	Ile	Pro	Lys
				515					520					525
Glu	Glu	Lys	Asp	Pro	Gly	Met	Gly	Ala	Met	Gly	Gly	Met	Gly	Gly
				530					535					540
Gly	Met	Gly	Gly	Gly	Met	Phe								
				545										

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 555

(B) TYPE: AMINO ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ala	Pro	His	Leu	Thr	Arg	Ala	Tyr	Ala	Lys	Asp	Val	Lys	Phe	Gly
1				5					10					15
Ala	Asp	Ala	Arg	Ala	Leu	Met	Leu	Gln	Gly	Val	Asp	Leu	Leu	Ala
				20					25					30
Asp	Ala	Val	Ala	Val	Thr	Met	Gly	Pro	Lys	Gly	Arg	Thr	Val	Ile
				35					40					45
Ile	Glu	Gln	Ser	Trp	Gly	Ser	Pro	Lys	Val	Thr	Lys	Asp	Gly	Val
				50					55					60
Thr	Val	Ala	Lys	Ser	Ile	Asp	Leu	Lys	Asp	Lys	Tyr	Lys	Asn	Ile
				65					70					75
Gly	Ala	Lys	Leu	Val	Gln	Asp	Val	Ala	Asn	Asn	Thr	Asn	Glu	Glu
				80					85					90
Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Arg	Ser	Ile
				95					100					105
Ala	Lys	Glu	Gly	Phe	Glu	Lys	Ile	Ser	Lys	Gly	Ala	Asn	Pro	Val
				110					115					120

Glu	Ile	Arg	Arg	Gly	Val	Met	Leu	Ala	Val	Asp	Ala	Val	Ile	Ala	125	130	135
Glu	Leu	Lys	Lys	Gln	Ser	Lys	Pro	Val	Thr	Thr	Pro	Glu	Glu	Ile	140	145	150
Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala	Asn	Gly	Asp	Lys	Asp	Ile	Gly	155	160	165
Asn	Ile	Ile	Ser	Asp	Ala	Met	Lys	Lys	Val	Gly	Arg	Lys	Gly	Val	170	175	180
Ile	Thr	Val	Lys	Asp	Gly	Lys	Thr	Leu	Asn	Asp	Glu	Leu	Glu	Ile	185	190	195
Ile	Glu	Gly	Met	Lys	Phe	Asp	Arg	Gly	Tyr	Ile	Ser	Pro	Tyr	Phe	200	205	210
Ile	Asn	Thr	Ser	Lys	Gly	Gln	Lys	Cys	Glu	Phe	Gln	Asp	Ala	Tyr	215	220	225
Val	Leu	Leu	Ser	Glu	Lys	Lys	Phe	Ser	Ser	Val	Gln	Ser	Ile	Val	230	235	240
Pro	Ala	Leu	Glu	Ile	Ala	Asn	Ala	His	Arg	Lys	Pro	Leu	Val	Ile	245	250	255
Ile	Ala	Glu	Asp	Val	Asp	Gly	Glu	Ala	Leu	Ser	Thr	Leu	Val	Leu	260	265	270
Asn	Arg	Leu	Lys	Val	Gly	Leu	Gln	Val	Val	Ala	Val	Lys	Ala	Pro	275	280	285
Gly	Phe	Gly	Asp	Asn	Arg	Lys	Asn	Gln	Leu	Lys	Asp	Met	Ala	Ile	290	295	300
Ala	Thr	Gly	Gly	Ala	Val	Phe	Gly	Glu	Glu	Gly	Leu	Asn	Leu	Asn	305	310	315
Leu	Glu	Asp	Val	Gln	Ala	His	Asp	Leu	Gly	Lys	Val	Gly	Glu	Val	320	325	330
Ile	Val	Thr	Lys	Asp	Asp	Ala	Met	Leu	Leu	Lys	Gly	Lys	Gly	Asp	335	340	345
Lys	Ala	His	Ile	Glu	Lys	Arg	Ile	Gln	Glu	Ile	Thr	Glu	Gln	Leu	350	355	360
Asp	Ile	Thr	Thr	Ser	Glu	Tyr	Glu	Lys	Glu	Lys	Leu	Asn	Glu	Arg	365	370	375

Leu Ala Lys Leu Ser Asp Gly Val Ala Val Leu Lys Val Gly Gly
 380 385 390
 Thr Ser Asp Val Glu Val Asn Glu Lys Lys Asp Arg Val Thr Asp
 395 400 405
 Ala Leu Asn Ala Thr Arg Ala Ala Val Glu Glu Gly Ile Val Leu
 410 415 420
 Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile Pro Ala Leu Asp Ser
 425 430 435
 Leu Lys Pro Ala Asn Glu Asp Gln Lys Ile Gly Ile Glu Ile Ile
 440 445 450
 Lys Arg Ala Leu Lys Ile Pro Ala Met Thr Ile Ala Lys Asn Ala
 455 460 465
 Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Leu Gln Ser Ser
 470 475 480
 Ser Glu Val Gly Tyr Asp Ala Met Leu Gly Asp Phe Val Asn Met
 485 490 495
 Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
 500 505 510
 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu
 515 520 525
 Ala Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met
 530 535 540
 Gly Ala Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe
 545 550 555
